

74. (Currently amended) A method for purifying tubulin comprising:

- a) contacting a sample containing tubulin with a support to which is attached a first peptide consisting of an amino acid sequence of RSSLIR (**SEQ ID NO: 7**) and a second peptide consisting of an amino acid sequence of SVRGSQ (**SEQ ID NO: 8**), wherein the contacting is under conditions enabling binding between the support and the tubulin in the same;
- b) rinsing the sample-contacted support to remove unbound molecules in said sample; and
- c) eluting said tubulin bound to said support;  
wherein said tubulin eluted from said support is purified.

**In the Abstract:**

Please delete the Abstract and replace it with the following Abstract:

The invention relates to protein-protein interactions and methods for identifying interacting proteins and the amino acid sequence at the site of interaction. Using overlapping hexapeptides that encode for the entire amino acid sequences of the linker domains of human P-glycoprotein gene 1 and 3 (HP-gp1 and HP-gp3), a direct and specific binding between HP-gp1 and 3 linker domains and intracellular proteins was demonstrated. Three different stretches (<sup>617</sup>EKGIFYFKLVTM<sup>627</sup>, (SEQ ID NO: 1)  
<sup>658</sup>SRSSLIRKRSTRRSVRGSQA<sup>677</sup> (**SEQ ID NO: 2**) and <sup>694</sup>PVSFWRIMKLNLT<sup>706</sup>  
(**SEQ ID NO: 3**) for HP-gp1 and <sup>618</sup>LMKKEGVYFKLVNM<sup>631</sup>, (**SEQ ID NO: 4**)  
<sup>648</sup>KAATRMAPNGWKSRLFRHSTQKNLKNS<sup>674</sup> (**SEQ ID NO: 5**) and  
<sup>695</sup>PVSFLKVLKLNKT<sup>707</sup> (**SEQ ID NO: 6**) for HP-gp3) in linker domains bound to proteins with apparent molecular masses of ~80 kDa, 57 kDa and 30 kDa. The binding of the 57 kDa protein was further characterized. Purification and partial N-terminal amino acid sequencing of the 57 kDa protein showed that it encodes the N-terminal amino acids of alpha and beta-tubulins. The method of the present invention was further validated with Annexin. The present invention thus demonstrates a novel concept whereby the interactions between two proteins are mediated by strings of few amino acids with high and repulsive binding energies, enabling the identification of high affinity binding sites between any interacting proteins.